

GenCore version 5.1.4-p5-4578  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OK protein - protein search, using sw model

Run on: May 16, 2003, 10:35:35 ; Search time 28 Seconds  
(without alignments)  
88.306 Million cell updates/sec.

Title: US-09-551-151A-43

Perfect score: 64

Sequence: 1 SPOGIACQRMFN 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4583

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mmc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	42.2	17	6	046473
2	25	39.1	13	4	P82276
3	23	35.9	8	5	P83316
4	23	35.9	10	5	P83280
5	22	34.4	10	2	Q9X3M2
6	22	34.4	11	2	Q9S623
7	22	34.4	13	2	Q9X3E1
8	22	34.4	13	2	Q9X3J6
9	22	34.4	13	4	Q8WY56
10	22	34.4	13	10	Q9S8V7
11	22	34.4	16	5	Q9TWK0
12	22	34.4	17	2	Q9X3I3
13	22	34.4	18	2	Q9X3H7
14	21	32.8	9	5	P83279
15	21	32.8	15	8	P82135
16	21	32.8	16	5	Q9TWK1

17	21	32.8	17	4	Q9UC72	Q9UC72 homo sapien
18	20	31.2	8	2	Q9X3K1	Q9X3K1 prochloroco
19	20	31.2	11	2	Q9A1Z8	Q9A1Z8 carsonella
20	20	31.2	12	12	Q86570	Q86570 hepatitis d
21	20	31.2	13	4	Q9UJ73	Q9UJ73 homo sapien
22	20	31.2	15	2	Q9R586	Q9R586 serralia ma
23	20	31.2	15	12	Q9PXC5	Q9PXC5 tobacco etc
24	20	31.2	17	4	Q9UC89	Q9UC89 homo sapien
25	20	31.2	17	10	P82947	P82947 glycine max
26	20	31.2	18	2	Q9R4F3	Q9R4F3 escherichia
27	20	31.2	18	4	Q9UE43	Q9UE43 homo sapien
28	20	31.2	18	4	Q9UE38	Q9UE38 homo sapien
29	20	31.2	18	5	Q9TWV6	Q9TWV6 aplysia cal
30	19.5	30.5	14	2	Q9R517	Q9R517 escherichia
31	19	29.7	9	4	Q14715	Q14715 homo sapien
32	19	29.7	10	11	Q9QVE6	Q9QVE6 mus sp. pro
33	19	29.7	14	2	P83077	P83077 bacillus ce
34	19	29.7	15	2	P83069	P83069 bacillus ce
35	19	29.7	15	4	Q9UC90	Q9UC90 homo sapien
36	19	29.7	16	4	Q9UC88	Q9UC88 homo sapien
37	19	29.7	16	11	Q9QUM5	Q9QUM5 rattus sp.
38	19	29.7	18	4	Q9POM3	Q9POM3 homo sapien
39	19	29.7	18	5	Q9TWM9	Q9TWM9 tetrahymena
40	18.5	28.1	18	4	Q8WY56	Q8WY56 homo sapien
41	18	28.1	10	2	Q9R7J8	Q9R7J8 helicobacte
42	18	28.1	10	13	Q9QY93	Q9QY93 gallus gall
43	18	28.1	11	2	Q47567	Q47567 escherichia
44	18	28.1	11	11	Q8R2J7	Q8R2J7 mesocricetu
45	18	28.1	12	4	Q9UMQ9	Q9UMQ9 homo sapien

## ALIGNMENTS

## RESULT 1

ID AC 046473 PRELIMINARY; PRT; 17 AA.  
AC 046473;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Lactase dehydrogenase A (Fragment).  
GN LDHA.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DOMESTICUS;  
RX MEDLINE=97141918; PubMed=8988168;  
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,  
O'Brien S.J.;  
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of  
mammalian genomes";  
RL Nat. Genet. 15:47-56(1997).  
DR EMBL; AF012095; AAC00072.2;  
FT NON\_TER 1 17  
FT NON\_TER 1 17  
SQ SEQUENCE 17 AA: 2018 MW: E47943B2E187C1FC CRC64;

Query Match 42.2% Score 27; DB 6; Length 17;  
Best Local Similarity 83.3% Pred. No. 2.4e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GQRNFN 12  
|||  
Db 3 GQRNFN 8

RESULT 2  
P82276 PRELIMINARY; PRT; 13 AA.  
ID P82276

```

AC P82276;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Tubulin-associated peptide (Fragment).
OC Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Rosbacher J., Gartner W., Kallinger H., Wagner L.;
RT "Haptoglobin mediated changes in cellular immune response.";
RL Submitted (JAN-2000) to the SWISS-PROT data bank.
CC -1- TISSUE SPECIFICITY: LEUKOCYTES AND HEPATOCYTES.
KW Microtubules.
FT NON_TER 1
FT TER 13
SQ SEQUENCE 13 AA; 1300 MW; 4FD05B1E478D62C7 CRC64;

Query Match 39.1%; Score 25; DB 4; Length 13;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 GORNF 10
DB 5 GVGQEN 11

RESULT 3
P83316 PRELIMINARY; PRT; 8 AA.
ID P83316;
AC P83316;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE FMRamide-like neuropeptide Flrp (GDRNFLRF-amide).
OS Pennaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Pennaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-EYESTALK;
RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
RA Chaisituthangkura P., Sithigorngul W., Petsom A.;
RT "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Pennaeus monodon.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
CC -1- MASS SPECTROMETRY: MW=1024.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 8
FT SEQUENCE 8 AA; 1024 MW; 72D40729C4540A8 CRC64;

Query Match 35.9%; Score 23; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11
DB 1 GDRNF 5

RESULT 4
P83280 PRELIMINARY; PRT; 10 AA.
ID P83280;
AC P83280;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Cytochrome b (Fragment).
GN PEBT.
OS Prochlorococcus sp.

```

```

DE FMRamide-like neuropeptide Flrp7 (GYDRNFLRF-amide).
OC Macrobrachium rosenbergii (Giant fresh water prawn).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-EYESTALK;
RA Sithigorngul P., Sarathongkum W., Longyant S., Panchan N.,
RA Sithigorngul W., Petsom A.;
RT "Three more novel FMRamide-like neuropeptide sequences from the
eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10
FT SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;

Query Match 35.9%; Score 23; DB 5; Length 10;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11
DB 3 GDRNF 7

RESULT 5
O9X3M2 PRELIMINARY; PRT; 10 AA.
ID O9X3M2;
AC O9X3M2;
DT 01-NOV-1998 (TREMBlrel. 12, Created)
DT 01-NOV-1998 (TREMBlrel. 12, Last sequence update)
DE Cytochrome b (Fragment).
GN PEBT.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).
DR EMBL; AF070219; AAD33269.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1076 MW; 75CA5C80586BD324 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GGIAG 7
DB 5 GDISG 9

RESULT 6
O9S623 PRELIMINARY; PRT; 11 AA.
ID O9S623;
AC O9S623;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Cytochrome b (Fragment).
GN PEBT.
OS Prochlorococcus sp.

```

OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus;  
 OC NCBI\_TaxID=1220;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream."  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL: AF070168; AAD23221.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 11 AA; 1153 MW; 5F551A5CB05866D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 11;  
 Best Local Similarity 80.0%; Pred. No. 1.4e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7  
 DB 5 OG1SG 9

RESULT 7  
 OY3X3E1 PRELIMINARY; PRT; 13 AA.  
 AC OY3X3E1;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN PETB.  
 OS Prochlorococcus sp.  
 OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus;  
 OC NCBI\_TaxID=1220;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream."  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL: AF070141; AAD20755.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1434 MW; 57EBE8029A866D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7  
 DB 7 OG1SG 11

RESULT 8  
 OY3X3J6 PRELIMINARY; PRT; 13 AA.  
 AC OY3X3J6;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE Cytochrome b (Fragment).  
 GN PETB.  
 OS Prochlorococcus sp.  
 OC Bacteria: Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus;  
 OC NCBI\_TaxID=1220;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream."  
 RL Limnol. Oceanogr. 43:1615-1630(1998).

DR EMBL: AF070189; AAD23225.1; -;  
 FT NON\_TER 1  
 SQ SEQUENCE 13 AA; 1473 MW; 57FA9A029A8666D3 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OG1AG 7  
 DB 7 OG1SG 11

RESULT 9  
 OY3W56 PRELIMINARY; PRT; 13 AA.  
 AC OY3W56;  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Epithelial sodium channel beta-3 subunit (Fragment).  
 GN SCN1B.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;  
 RT "Genomic organization of the 5' end of human beta ENaC and preliminary  
 characterization of its promoter."  
 RL Am. J. Physiol. Renal Physiol. 0:0-0(2002).  
 DR EMBL: AF260228; AAL48197.1; -;  
 KW Ionic channel.  
 FT NON\_TER 13  
 SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;

Query Match 34.4%; Score 22; DB 4; Length 13;  
 Best Local Similarity 50.0%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 GIACGRNF 11  
 DB 5 GNLGDKNF 12

RESULT 10  
 OY3S8V7 PRELIMINARY; PRT; 15 AA.  
 AC OY3S8V7;  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
 DE High-molecular-weight glutenin subunit (Fragment).  
 OS Triticum aestivum (Wheat).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticaceae; Triticum.  
 OC NCBI\_TaxID=4565;  
 RN (1)  
 RP SEQUENCE.  
 RX MEDLINE=93003354; PubMed=1390908;  
 RA Tao H.P., Adalstein A.E., Kasarda D.D.;  
 RT "Intermolecular disulfide bonds link specific high-molecular-weight  
 glutenin subunits in wheat endosperm."  
 RL Biochim. Biophys. Acta 1159:13-21(1992).  
 SQ SEQUENCE 15 AA; 1559 MW; CD1A6F573C945AFD CRC64;

Query Match 34.4%; Score 22; DB 10; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PG1AG 7

Db 4 POGXOG 9

## RESULT 11

OGTAKO PRELIMINARY; PRT; 16 AA.  
 ID OGTAKO  
 AC OGTAKO  
 DT 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Proximal collagen (Fragment).  
 OS Mytilus edulis (Blue mussel).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;  
 OC Mytiloidea; Mytilidae; Mytilus.  
 OX NCBI\_TaxID=6550;  
 RN [1]  
 RP SEQUENCE  
 RX MEDLINE=95230211; PubMed=7714453;  
 RA Qin X., Waite J.H.;  
 RT "Exotic collagen gradients in the byssus of the mussel Mytilus  
 edulis";  
 RL J. Exp. Biol. 198;633-644(1995).  
 SQ SEQUENCE 16 AA; 1347 MM; B57F18783A18783C CRC64;

Query Match 34.4%; Score 22; DB 5; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 POGIAG 7  
 Db 5 POGAEG 10

## RESULT 12

OGX313 PRELIMINARY; PRT; 17 AA.  
 ID OGX313  
 AC OGX313  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DE Cytochrome b (Fragment).  
 OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream";  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070176; AAD20791.1;  
 FT NON\_TER  
 SQ SEQUENCE 17 AA; 1953 MM; 630843039ADD51B4 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 17;  
 Best Local Similarity 80.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OGIAIG 7  
 Db 11 OGISG 15

## RESULT 13

OGX3H7 PRELIMINARY; PRT; 18 AA.  
 ID OGX3H7  
 AC OGX3H7  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE Cytochrome b (Fragment).  
 GN PEB.

OS Prochlorococcus sp.  
 OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
 OC Prochlorococcus.  
 OX NCBI\_TaxID=1220;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urbach E., Chisholm S.W.;  
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically  
 sorted from the Sargasso Sea and Gulf Stream";  
 RL Limnol. Oceanogr. 43:1615-1630(1998).  
 DR EMBL; AF070170; AAD20782.1;  
 FT NON\_TER  
 SQ SEQUENCE 18 AA; 2117 MM; 09842D229ADD51A5 CRC64;

Query Match 34.4%; Score 22; DB 2; Length 18;  
 Best Local Similarity 80.0%; Pred. No. 2.4e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 OGIAIG 7  
 Db 12 OGISG 16

## RESULT 14

P83279 PRELIMINARY; PRT; 9 AA.  
 ID P83279  
 AC P83279  
 DT 01-MAR-2002 (TREMBlrel. 20, Created)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE FMRFamide-like neuropeptide FLP6 (DSGRNFRF-amide).  
 OS Macrobrachium rosenbergii (Giant fresh water prawn).  
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;  
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;  
 OC Palaemonoidea; Palaemonidae; Macrobrachium.  
 OX NCBI\_TaxID=79674;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-EYE/STALK.  
 RX MEDLINE=21107394; PubMed=11179812;  
 RA Sthigornigul P., Sarathkum W., Longyant S., Panchan N.,  
 RA Sthigornigul W., Petson A.;  
 RT "Three more novel FMRFamide-like neuropeptide sequences from the  
 eyestalk of the giant freshwater prawn Macrobrachium rosenbergii";  
 RL Peptides 22:191-197(2001).  
 CC -1- MASS SPECTROMETRY: MW=1080.7; METHOD=MALDI.  
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)  
 CC FAMILY.  
 CC Neuropeptide; Amidation.  
 KW MOD\_RES  
 FT MOD\_RES  
 SQ SEQUENCE 9 AA; 1081 MM; 26800729CA540878 CRC64;

Query Match 32.8%; Score 21; DB 5; Length 9;  
 Best Local Similarity 80.0%; Pred. No. 6.7e+05;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 7 GORNF 11  
 Db 2 GGRNF 6

## RESULT 15

P82135 PRELIMINARY; PRT; 15 AA.  
 ID P82135  
 AC P82135  
 DT 01-JUN-2000 (TREMBlrel. 14, Created)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)  
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)  
 DE Chloroplast 30S ribosomal protein S18 alpha (Fragment).  
 OS Spinacia oleracea (Spinach).  
 OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.  
 OX NCBI\_TaxID=3562;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC STRAIN-CV. ALVARO; TISSUE-LEAF;  
 RX MEDLINE=20435797; PubMed=10874039;  
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;  
 RT "The plastid ribosomal proteins. Identification of all the proteins in  
 the small subunit of an organelle ribosome (chloroplast).";  
 RL J. Biol. Chem. 37:28455-28465(2000).  
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
 CC -1- MISCELLANEOUS: S18 ALPHA AND BETA FORMS DIFFER IN PI. S18 BETA  
 CC FORM IS THE LEAST BASIC FORM.  
 CC -1- MASS SPECTROMETRY: MW=12093; METHOD-MALDI.  
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.  
 CC -1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.  
 DR InterPro: IPR001648; Ribosomal\_S18.  
 DR Pfam: PF01084; Ribosomal\_S18; PARTIAL.  
 DR PROSITE: PS00057; RIBOSOMAL\_S18; PARTIAL.  
 KW Ribosomal protein; Chloroplast.  
 FT NON\_TER 15 15  
 SQ SEQUENCE 15 AA; 1910 MW; C29396E592403B60 CRC64;

## Query Match

32.8%; Score 21; DB 8; Length 15;

Best Local Similarity 57.1%; Pred. No. 3.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 TAGQRNF 11  
 I :|||  
 DB 9 IKRRNF 15

Search completed: May 16, 2003, 10:38:03  
 Job time : 29 secs

